Modeling Spatial Correlation of Transcripts with Application to Developing Pancreas.

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Public Summary:

Scientific Abstract:
Recently high-throughput image-based transcriptomic methods were developed and enabled researchers to spatially resolve gene expression variation at the molecular level for the first time. In this work, we develop a general analysis tool to quantitatively study the spatial correlations of gene expression in fixed tissue sections. As an illustration, we analyze the spatial distribution of single mRNA molecules measured by in situ sequencing on human fetal pancreas at three developmental time points-80, 87 and 117 days post-fertilization. We develop a density profile-based method to capture the spatial relationship between gene expression and other morphological features of the tissue sample such as position of nuclei and endocrine cells of the pancreas. In addition, we build a statistical model to characterize correlations in the spatial distribution of the expression level among different genes. This model enables us to infer the inhibitory and clustering effects throughout different time points. Our analysis framework is applicable to a wide variety of spatially-resolved transcriptomic data to derive biological insights.